

GenCore version 5.1.9
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QM nucleic - protein search, using frame_plus_n2p model
 Run on: July 11, 2006, 17:21:18 ; Search time 30.5853 Seconds
 (without alignments)
 3284.476 Million cell updates/sec

Title: US-10-646-950-6
 Perfect score: 645
 Sequence: 1 cattattagccagatgaa.....gagagacttcaagcttcaa 362
 Scoring table: BLOSUM62
 Xgapop 10.0 , Xgapext 0.5
 Ygapop 10.0 , Ygapext 0.5
 Fgapop 6.0 , Fgapext 7.0
 Delop 6.0 , Delext 7.0

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 5699196

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0*
 Maximum Match 100*
 Listing first 45 summaries

Command line parameters:
 -MODEL:frame+_n2p,model=-DEV-xlp
 -Q=abes/ABSWEB_spool/US10646950/runat_11072006_111734_6250/app_query.fasta_1
 -DB=UniProt -QFMT=fastaN -SUFFIX=n2p.rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
 -UNIT=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
 -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MAXLEN=2000000000 -HOST=abes02p
 -USER=US10646950 -CGN_1_1_762 .runat_11072006_111734_6250 -NCPU=6 -ICPU=3
 -NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
 -YGAPOP=10 -YGAPEXT=0 -DELOP=6 -DELEXT=7

Database : UniProt_7.2:
 1: uniprot_sprot:
 2: uniprot_trembl:
 *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query				Description
No.	Score	Match	Length	DB ID	
1	567	87.9	475	1 FACE1_HUMAN	Q75844 homo sapien
2	558	86.5	475	1 FACE1_MOUSE	Q80w54 mus musculus
3	554	85.9	493	2 Q5R6Y6_PONPY	Q5r6y6 pongo pygmaeus
4	533	82.6	465	2 Q640V5_XENLA	Q640V5 xenopus laevis
5	510	79.1	468	2 Q80221_BRARE	Q80221 brachydanius
6	509	78.9	485	2 Q4RMb6_TEITNG	Q4rm66 tetraodon nigriventer
7	317.5	49.2	126	2 Q5BKK4_SCHJA	Q5bkk4 schistosoma haematobium
8	304.5	47.2	472	2 Q3Y6B8_TAESO	Q3y6b8 taenia solium
9	296.5	46.0	451	2 Q9V7W7_DROME	Q9v7w7 drosophila melanogaster
10	271.5	42.1	394	2 Q5TSY1_ANOGA	Q5tsy1 anopheles gambiae
11	271.5	42.1	453	2 Q7QA21_ANOGA	Q7qa21 anopheles gambiae
12	243	37.7	425	2 Q6EPN8_ORYSA	Q6epn8 oryza sativa
13	242.5	37.6	456	2 Q2UGJ7_ASPOR	Q2ugj7 aspergillus
14	240.5	37.3	460	2 Q55UG3_CRYNE	Q55ug3 cryptococcus
15	240.5	37.3	460	2 Q5KHY1_CRYNE	Q5khy1 cryptococcus

16	237	36.7	424	2	Q8RX88_ARATH	Q8rx88 arabidopsis
17	237	36.7	424	2	Q93ZV9_ARATH	Q93zv9 arabidopsis
18	236.5	36.7	479	2	Q4WP06_ASPLFU	Q4wp06 aspergillus
19	234.5	36.4	456	2	Q7ST78_EEMENI	Q7s178 emericella
20	233	36.1	424	2	Q94F88_ARATH	Q94f88 arabidopsis
21	231.5	35.9	442	2	Q7RVV7_NEUCCR	Q7rvv7 neurospora
22	231.5	35.9	446	2	Q6BMD9_DEBHA	Q6bmd9 debaryomyce
23	231.5	35.9	462	2	Q9C2C0_NEUCCR	Q9c2c0 neurospora
24	229.5	35.6	867	2	Q4IA57_GIBZ	Q4ia57 gibberella
25	223.5	34.7	456	2	Q59UR6_CANAL	Q59ur6 candida alb
26	223.5	34.7	456	2	Q81HA2_DROME	Q81ha2 drosophila
27	220.5	34.2	447	2	Q9V7W6_DROME	Q9v7w6 drosophila
28	217.5	33.7	453	2	Q56D07_PARB	Q56d07 paracoccidi
29	213	33.0	455	2	Q9M139_ARATH	Q9m139 arabidopsis
30	211.5	32.8	442	2	Q61LX2_CAEHR	Q61lx2 caenorhabdi
31	204.5	31.7	442	2	Q9XVE5_CAEEL	Q9xve5 caenorhabdi
32	190.5	29.5	453	1	STE24_YEAST	P47154 saccharomy
33	189.5	29.4	474	1	STE24_SCHPO	Q10071 schizosacch
34	185	28.7	419	2	Q967X5_PHYPO	Q967x5 physarum po
35	176.5	27.4	456	2	Q6CR94_KLUL4	Q6cr94 kluyveromy
36	174	27.0	426	2	Q54FH7_DICD1	Q54fh7 dictyosteli
37	173.5	26.9	456	2	Q9V7W5_DROME	Q9v7w5 drosophila
38	169.5	26.3	444	2	Q4N3R0_THEPA	Q4n3r0 theileria p
39	167.5	26.0	438	2	Q4UFQ9_THEAN	Q4ufq9 theileria a
40	166.5	25.8	316	2	Q04602_ARATH	Q04602 arabidopsis
41	161.5	25.0	460	2	Q6FQ89_CANGA	Q6fq89 candida gla
42	156.5	24.3	422	2	Q3ASZ1_CHLCH	Q3a2z1 chlorobium
43	156.5	24.3	427	2	Q3BE89_9TRYP	Q3be89 trypanosoma
44	156.5	24.3	453	2	Q2LYG7_9DELT	Q2lyg7 syntrophus
45	153	23.7	410	2	Q3XRV0_9PROT	Q3xrv0 magnetococc

ALIGNMENTS

RESULT 1

FACE1_HUMAN

ID FACE1_HUMAN STANDARD; PRT; 475 AA.

AC Q75844; Q8ND28; Q9UBQ2;

DT 15-JUL-1999, integrated into UniProtKB/Swiss-Prot.

DT 27-APR-2001, sequence version 2.

DT 07-FEB-2006, entry version 50.

DE CAAK prenyl protein-1 homolog (EC 3.4.24.84) (Prenyl protein-specific metalloprotease 1) (farnesylated protein-converting enzyme 1) (FACE-1)

DE (Zinc metalloproteinase Ste24 homolog).

GN Name=ZMPSTE24; Synonyms=FACE1, STE24;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OK NCBI_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE [mRNA].

RC TISSUE=Brain;

RX MEDLINE=9177429; PubMed=10076063; DOI=10.1016/S0304-4165(98)00170-6;

RA Kumagai H., Kawamura Y., Yanagisawa K., Komano H.;

RT "Identification of a human cDNA encoding a novel protein structurally related to the yeast membrane-associated metalloprotease, Ste24p.";

RL Biochim. Biophys. Acta 1426:1468-474(1999).

RN [2]

RP NUCLEOTIDE SEQUENCE [mRNA].

RC TISSUE=B-cell, and Fetal brain;

RX MEDLINE=98365461; PubMed=9700155; DOI=10.1083/jcb.142.3.635;

RA Tam A., Nouvet F.J., Fujimura-Kamada K., Slunt H., Sisodia S.S., Michaelis S.;

RT Dual roles for Ste24p in yeast a-factor maturation: NH2-terminal proteolysis and COOH-terminal CAAK processing.;

RL J. Cell Biol. 142:635-649(1998).

RN [3]

RP NUCLEOTIDE SEQUENCE [mRNA].

RC TISSUE=Ovary;

RX MEDLINE=99303558; PubMed=10373325; DOI=10.1006/geno.1999.5834;

RA Freije J.M.P., Blay P., Pendas A.M., Cadinanos J., Crespo P., Lopez-Otin C.;
RT "Identification and chromosomal location of two human genes encoding
RT enzymes potentially involved in proteolytic maturation of farnesylated
RT proteins.";
RL Genomics 58:270-280(1999).
RN [4]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RG Human chromosome 1 international sequencing consortium;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE mRNA].
RC TISSUE=Testis;
RX MEDLINE-22388257; PubMed-12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D.,
RA Altshuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Dlatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Reha S., Loguercio N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketheman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smilus D.E.,
RA Scherzer A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [6]
RP VARIANT MADE ARG-340.
RX MEDLINE-22793839; PubMed-12913070; DOI=10.1093/hmg/ddg213;
RA Agarwal A.K., Fryns J.-P., Auchus R.J., Garg A.;
RT "Zinc metalloproteinase, ZMPSTE24, is mutated in mandibuloacral
RT dysplasia";
RL Hum. Mol. Genet. 12:1995-2001(2003).
CC -!- FUNCTION: Proteolytically removes the C-terminal three residues of
CC farnesylated proteins. Acts on lamin A/C.
CC -!- CATALYTIC ACTIVITY: The peptide bond hydrolyzed can be designated
CC -C-|A-A-X in which C is an S-isoprenylated cysteine residue, A is
CC usually aliphatic and X is the C-terminal residue of the substrate
CC protein, and may be any of several amino acids.
CC -!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
CC reticulum and possibly also the Golgi compartment.
CC -!- TISSUE SPECIFICITY: Widely expressed. High levels in kidney,
CC prostate, testis and ovary.
CC -!- DISEASE: Defects in ZMPSTE24 are the cause of mandibuloacral
CC dysplasia with type B lipodystrophy (MADB) [MIM:608612].
CC Mandibuloacral dysplasia (MAD) is a rare autosomal recessive
CC disorder characterized by mandibular and clavicular hypoplasia,
CC acroosteolysis, delayed closure of the cranial suture, joint
CC contractures, and types A or B patterns of lipodystrophy. Type B
CC lipodystrophy observed in MADB, is characterized by generalized
CC fat loss.
CC -!- SIMILARITY: Belongs to the peptidase M48A family.
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
DR EMBL; AB016068; BAA33727.1; -; mRNA.
DR EMBL; AF064867; AAC68866.1; -; mRNA.
DR EMBL; Y13834; CAB46277.1; -; mRNA.
DR EMBL; AL050341; CAB81610.1; -; Genomic_DNA.
DR EMBL; BC037283; AAH37283.1; -; mRNA.
DR MEROPS; M48.003; -.

DR Ensembl; ENSG0000084073; Homo sapiens.
 DR HGNC; HGNC:12877; ZMPSTE24.
 DR MIM; 606480; gene.
 DR MIM; 608612; phenotype.
 DR GO; GO:0008235; Fimetalloexopeptidase activity; TAS.
 DR GO; GO:0006508; Proteolysis and peptidolysis; TAS.
 DR InterPro; IPR006025; Pept_M_Zn_RS.
 DR InterPro; IPR001915; Peptidase_M48.
 DR Pfam; PF0143; Peptidase_M48; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; FALSE_NEG.
 KW Disease mutation; Endoplasmic reticulum; Golgi stack; Hydrolase;
 KW Membrane; Metal-binding; Metalloprotease; Protease; Transmembrane;
 KW Zinc.
 FT CHAIN 1 475 CAACT prenyl protease 1 homolog.
 FT /FTId-PRO_0000138844.
 FT TRANSMEM 19 39 Potential.
 FT TRANSMEM 82 102 Potential.
 FT TRANSMEM 124 144 Potential.
 FT TRANSMEM 171 191 Potential.
 FT TRANSMEM 196 216 Potential.
 FT TRANSMEM 348 368 Potential.
 FT TRANSMEM 383 405 Potential.
 FT ACT_SITE 336 336 By similarity.
 FT ACT_SITE 419 419 Proton donor (By similarity).
 FT METAL 335 335 Zinc (catalytic) (By similarity).
 FT METAL 339 339 Zinc (catalytic) (By similarity).
 FT METAL 415 415 Zinc (catalytic) (By similarity).
 FT VARIANT 340 340 W -> R (in MADB).
 FT /FTId-VAR_019308.
 FT CONFLICT 16 16 E -> K (in Ref. 1).
 FT CONFLICT 137 137 T -> A (in Ref. 5; AAH37283).
 SQ SEQUENCE 475 AA; 54813 MW; 6C49179DEB0C8F7F CRC64;

Alignment Scores:

Pred. No.:	9.88e-64	Length:	475
Score:	567.00	Matches:	115
Percent Similarity:	95.8%	Conservative:	0
Best Local Similarity:	95.8%	Mismatches:	5
Query Match:	87.9%	Indels:	1
DB:	1	Gaps:	0

US-10-646-950-6 (1-362) x FACE1_HUMAN (1-475)

QY	2 ATTATTAGGCCAGATGAACTTCTTCTGTGTTTTTTATTGCTGTATTAAATGGTCA 61
Db	350 IleIleSerGlnMetAsnSerPheLeuCysPhePheLeuPheAlaValLeuIleGlyArg 369
QY	62 AAGGAGCTTTCTGCTGATTTGGTTTTATGNTAGCCAACCCACTNTTATTGGACTATIG 121
Db	370 LysGluLeuPheAlaAlaPheGlyPheTyrAspSerGlnProThrLeuIleGlyLeuLeu 389
QY	122 NTCATCTTCCAGTTTATTTTCACTTACAATGNGTTCTTCTTGTCTAACAGTC 181
Db	390 IleIlePheGlnPheIlePheSerProTyrAspGluValLeuSerPheCysLeuThrVal 409
QY	182 CTAAGCCGAGATTGAGTTCAAGCTGATGCATT-GCCAAGAACTTGGGAAGGCTAA 240
Db	410 LeuSerArgArgPheGluPheGlnAlaAspAlaPheAlaLysLeuGlyLysAlaLys 429
QY	241 GACTTATATTCTGCTTAAATCAAACCTAACAAAGATAACTTGGGATCCCTGTTCTGAC 300
Db	430 AspLeuTyrSerAlaLeuIleLysLeuAsnLysAspAsnLeuGlyPheProValSerAsp 449
QY	301 TGGTTGGTCTCAATGJGGCATTAATCTCATCCTCCACCTGCTAGAGAGACTTCAAGCTTG 360
Db	450 TrpLeuPheSerMetTrpHisTyrSerHisProProLeuLeuGluArgLeuGlnAlaLeu 469